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<170>   PatentIn version 3.3

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Pro Glu Gly Tyr Val Glu Gln Leu Thr Gln Leu Met Glu His Gly Trp
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Ser Pro Glu Asn Gly Ala Arg Val Val Ala Lys Ala Trp Val Asp Pro
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Gln Phe Arg Ala Leu Leu Leu Lys Asp Gly Thr Ala Ala Cys Ala Gln
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ttc ggc tac acc ggc ccc cag ggc gaa tac atc gtt gcc ctg gag gat   291
Phe Gly Tyr Thr Gly Pro Gln Gly Glu Tyr Ile Val Ala Leu Glu Asp
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Thr Pro Thr Leu Lys Asn Val Ile Val Cys Ser Leu Cys Ser Cys Thr

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Gly Thr Glu Leu Pro Arg Asp Met Val Val Lys Val Trp Asp Thr Ser
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Ala Glu Ser Arg Tyr Leu Val Leu Pro Val Arg Pro Glu Gly Ser Glu
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His Met Ser Glu Glu Gln Leu Gln Ala Leu Val Thr Lys Asp Val Leu
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Ile Gly Val Ala Leu Pro Arg Val Gly
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                      Met Asp Gly Phe His Asp Leu Gly Gly Phe Gln
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Gly Phe Gly Lys Val Pro His Thr Ile Asn Ser Leu Ser Tyr Lys Gln
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Val Phe Lys Gln Asp Trp Glu His Leu Ala Tyr Ser Leu Met Phe Ile
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Gly Ala Asp His Leu Lys Lys Phe Ser Val Asp Glu Val Arg His Ala
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Thr Gln Ala Glu Leu Asp Gln Ala Leu Gly Ser His Phe Lys Leu Ala
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2

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Leu Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg
        35                  40                  45


Val Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Ala Leu Leu Leu
    50                  55                  60


Lys Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Tyr Thr Gly Pro Gln
65                  70                  75                  80


Gly Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Thr Leu Lys Asn Val
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Ile Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu
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6

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Pro Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg
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Glu Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Arg Asp
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Met Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val
145                 150                 155                 160

Leu Pro Val Arg Pro Glu Gly Ser Glu His Met Ser Glu Glu Gln Leu
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Val Gly
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Trp Glu His Leu Ala Tyr Ser Leu Met Phe Ile Gly Ala Asp His Leu
        35                  40                  45

Lys Lys Phe Ser Val Asp Glu Val Arg His Ala Val Glu Arg Leu Asp
    50                  55                  60

Val Arg Gln His Val Gly Thr Gln Tyr Tyr Glu Arg Tyr Val Ile Ala
65                  70                  75                  80

Thr Ala Thr Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu
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Asp Gln Ala Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala
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Glu Gly Arg Pro Ala Ile Thr Gly Arg Pro Pro Phe Glu Val Gly Asp
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Ala Tyr Val Arg Gly Lys Glu Gly Val Val Leu His Arg Thr Ser Glu
145                 150                 155                 160

Lys Trp Pro Phe Pro Asp Ala Ile Gly His Gly Asp Val Ser Ala Ala
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His Gln Pro Thr Tyr His Val Glu Phe Ala Val Lys Asp Leu Trp Gly
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            20                  25                  30

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Asn Arg Glu Gly Leu Arg Val Ala Val Ile Val Asn Asp Met Ser Glu
            35                  40                  45

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Val Asn Ile Asp Ala Glu Glu Val Gln Arg Asp Val Ala Leu His Arg
        50                  55                  60

ggt cgc gat gag ctg atc gag atg agc aac ggg tgc atc tgc tgc acc    240
Gly Arg Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
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8

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cgt ttc gat tac ctg ctg att gaa tcc acg ggg atc tcc gag ccg atg      336
Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
            100                 105                 110

ccg gtc gcg gag acg ttc gcc ttc ctt gac gct gat ggc ttc agc ctc      384
Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asp Gly Phe Ser Leu
            115                 120                 125

agc gaa ctg gcg cgc ctg gac acc ttg gtg acg gtg gtc gat ggc agt      432
Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Gly Ser
        130                 135                 140

cgt ttc cag gaa ctg ctc gaa tcg ccg cac acc gtt gac cag gat gac      480
Arg Phe Gln Glu Leu Leu Glu Ser Pro His Thr Val Asp Gln Asp Asp
145                 150                 155                 160

gcc acg cca gac gca ccc aag cgc cac ctg gcc gat ctg ctg atc gaa      528
Ala Thr Pro Asp Ala Pro Lys Arg His Leu Ala Asp Leu Leu Ile Glu
                165                 170                 175

cag gtg gag tac gcc aac gtc att ctc gtc aat aag ctg gat ctg atc      576
Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Leu Asp Leu Ile
            180                 185                 190

gat gca gcg cag tat cag gcc gtg cag gcg atc ctc aca ggc ctt aac      624
Asp Ala Ala Gln Tyr Gln Ala Val Gln Ala Ile Leu Thr Gly Leu Asn
        195                 200                 205

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Pro Thr Ala Arg Ile Met Pro Met Ala His Gly Asn Ile Pro Ser Ala
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ctg gaa acc ggc ctg ctg gtg caa agc ggc aag cgg ttc cag tgg gac      960
Leu Glu Thr Gly Leu Leu Val Gln Ser Gly Lys Arg Phe Gln Trp Asp
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tat gtc ggg cgc tgg tgg aac ttc atc gag ccg tcg caa tgg ccc cgg     1008
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9

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Asp Glu Tyr Arg Leu Gln Gly Ile Arg Ala Lys Trp Asp Ser Val Val
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Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu
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Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala
385             390             395             400

ttt gac cga cag acc ctt gcc cgc ccc cca cac agc cca tgg cga ttg   1248
Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu
                405             410             415

ccc cca ttt gat ccg aga tag                                        1269
Pro Pro Phe Asp Pro Arg
            420
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<210> 5
<211> 422
<212> PRT
<213> Pseudomonas marginalis

<400> 5

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Met Thr Asp Gly Ala Gln Ala Ser Arg Leu Pro Val Thr Val Leu Ser
1               5               10              15


Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
            20              25              30


Asn Arg Glu Gly Leu Arg Val Ala Val Ile Val Asn Asp Met Ser Glu
        35              40              45


Val Asn Ile Asp Ala Glu Glu Val Gln Arg Asp Val Ala Leu His Arg
    50              55              60


Gly Arg Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
65              70              75              80


Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Met Leu Ala Arg Gln Gln
            85              90              95


Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
```

10

100   105   110

        Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asp Gly Phe Ser Leu
                115   120   125

        Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Gly Ser
                130   135   140

        Arg Phe Gln Glu Leu Leu Glu Ser Pro His Thr Val Asp Gln Asp Asp
        145   150   155   160

        Ala Thr Pro Asp Ala Pro Lys Arg His Leu Ala Asp Leu Leu Ile Glu
                        165   170   175

        Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Leu Asp Leu Ile
                        180   185   190

        Asp Ala Ala Gln Tyr Gln Ala Val Gln Ala Ile Leu Thr Gly Leu Asn
                    195   200   205

        Pro Thr Ala Arg Ile Met Pro Met Ala His Gly Asn Ile Pro Ser Ala
            210   215   220

        Ser Leu Leu Gly Thr His Leu Phe Asp Leu Pro Ser Leu Ala Ala Ser
        225   230   235   240

        Pro Gly Trp Met Arg Lys Met Glu Ala Ala Asp Ala Pro Ala Ser Glu
                        245   250   255

        Ser Asp Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Glu Arg Ala Pro
                    260   265   270

        Phe His Pro Gln Arg Leu Leu Asp Phe Leu Gln Gln Pro Trp Cys Asn
                275   280   285

        Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
            290   295   300

        Leu Glu Thr Gly Leu Leu Val Gln Ser Gly Lys Arg Phe Gln Trp Asp
        305   310   315   320

        Tyr Val Gly Arg Trp Trp Asn Phe Ile Glu Pro Ser Gln Trp Pro Arg
                    325   330   335

        Asp Glu Tyr Arg Leu Gln Gly Ile Arg Ala Lys Trp Asp Ser Val Val

                                    11

```
                    340                    345                    350

        Gly Asp Cys Arg Gln Glu Leu Val Phe Ile Gly Gln Gly Leu Asp Thr
                355                    360                    365


        Asp Ala Leu Gln Arg Glu Leu Asp His Cys Leu Leu Ser Ala Gln Glu
            370                    375                    380
        Ile Ala Ala Gly Pro Leu Ala Trp Gln Ala Leu Pro Gly Ala Thr Ala
        385                    390                    395                    400


        Phe Asp Arg Gln Thr Leu Ala Arg Pro Pro His Ser Pro Trp Arg Leu
                405                    410                    415


        Pro Pro Phe Asp Pro Arg
                420


        <210>  6
        <211>  2371
        <212>  DNA
        <213>  Pseudomonas putida


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        <221>  CDS
        <222>  (1)..(582)
        <223>  Gen der Kodierregion der alpha-Untereinheit

        <220>
        <221>  CDS
        <222>  (624)..(1286)
        <223>  Gen der Kodierregion der beta-Untereinheit

        <220>
        <221>  gene
        <222>  (1283)..(2371)
        <223>  Gen des Aktivatorproteins

        <400>  6
        atg acg gca act tca acc cct ggt gag cgg gca cgc gca ttg ttt gca       48
        Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
        1                   5                   10                  15

        gtg ctc aag cgc aaa gac ctc atc ccc gag ggc tac atc gaa cag ctc       96
        Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
                        20                  25                  30

        acc cag ctg atg gaa cac ggc tgg agc ccg gaa aac ggc gcg cgc atc      144
        Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
                    35                  40                  45

        gtc gcc aag gcc tgg gtc gat ccg cag ttt cgc gag ctg ctg ctc aag      192
        Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys
            50                  55                  60

        gac ggt acg gcc gcc tgc gcc cag ttc ggc ttc acc ggc cca caa ggc      240
        Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
```

```
gaa tac atc gtc gcc ctg gaa gac acc ccg cag ttg aaa aac gtg atc          288
Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
                    85                  90                  95

gtc tgt agc ctg tgc tcc tgc acg aac tgg ccg gtg ctg ggc ctg cca          336
Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro
                100                 105                 110

cct gag tgg tac aag ggc ttc gag ttc cgt gcg cgg ttg gtc cgg gag          384
Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu
            115                 120                 125

ggg cgc acg gta ttg cgc gag ctg ggc acc gag ttg ccc ggc gac atg          432
Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met
        130                 135                 140

gtg gtc aag gtc tgg gac acc agc gct gaa agc cgc tac ctg gtg ctg          480
Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu
145                 150                 155                 160

ccg caa cga cca gcg ggc tca gag cat atg agc gaa gag cag ttg cgg          528
Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg
                165                 170                 175

caa ctg gtc acc aag gac gtg ctg atc ggc gtc gcc ctg ccc cgc gtt          576
Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val
                180                 185                 190

ggc tga gcaaggccgc ccaaccccat tcaacttccg gagtgttcaa t atg gat ggc        632
Gly                                                  Met Asp Gly
                                                             195

ttt cac gat ctc ggc ggt ttc cag ggc ttt ggc aaa gtg ccc cac cgc          680
Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val Pro His Arg
            200                 205                 210

atc aac agc ctg agc tac aag cag gtg ttc aag cag gac tgg gaa cac          728
Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp Trp Glu His
            215                 220                 225

ctg gcc tac agc ctg atg ttc atc ggc gtc gac cac ctg aac aag ttc          776
Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu Asn Lys Phe
        230                 235                 240

agc gtc gac gaa ata cgt cat gcc gtc gaa cgc att gac gtg cgc cag          824
Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp Val Arg Gln
245                 250                 255                 260

cac gtc ggc acc gaa tac tac gaa cgt tat gtg atc gcc act gcc acg          872
His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala Thr Ala Thr
                265                 270                 275

ctg ctg gtc gaa aca ggc gtc atc acc cag gcc gaa ctg gat gaa gca          920
Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu Asp Glu Ala
                280                 285                 290

ctc ggc tcg cac ttc aag ctg gcc aac ccc gcc cat gcg caa ggg cgt          968
Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala Gln Gly Arg
            295                 300                 305
```

13

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gct gca att atc ggg cga gcg cct ttt gaa gtg ggc gat cgg gtc atc    1016
Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp Arg Val Ile
    310             315             320

gta cgc gat gaa tac gtg gcc ggg cat gtg cgc atg cct gca tac gtg    1064
Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro Ala Tyr Val
325             330             335             340


cgc ggc aag caa ggc gta gtg ctg cac cgg acc act gaa cag tgg ccg    1112
Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu Gln Trp Pro
            345             350             355

ttt ccg gac gcg att ggc cat ggc gac cag agc gct gcg cat caa ccg    1160
Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala His Gln Pro
            360             365             370

acc tac cat gtc gag ttc cgc gtg cgg gac ctg tgg ggc gat gcc gca    1208
Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly Asp Ala Ala
            375             380             385

gac gac ggc ctg gtg gtg gta gac ctg ttc gaa agc tat ctg gac agg    1256
Asp Asp Gly Leu Val Val Val Asp Leu Phe Glu Ser Tyr Leu Asp Arg
    390             395             400

gtc gaa agc ccg cga gtg gtg cgc gca tga gtgccggcgc ccaggcaggc      1306
Val Glu Ser Pro Arg Val Val Arg Ala
405             410

cggctgccgg tgacggtcct ttcaggcttc ctcggcgcag gcaagaccac cctgctcaac   1366

cacatcctgc gcaaccgcca gggcctgaag gtggcggtta tcgtcaatga catgagcgag   1426

gtcaacatcg atgccgccca ggtccagcgc gacgttgcgc tgtatcgtgg ccaggatgaa   1486

ttgatagaga tgagcaacgg ctgtatctgc tgcaccctgc gcgccgacct gcttgagcag   1546

atcagcgcgc tggcgcgcca gcagcgtttc gattacctgt tgatcgagtc caccgggatt   1606

tccgagccga tgccagtcgc cgagaccttt gcctttctcg acgccaacgg tttcagcctc   1666

agcgaactgg cgcggctgga tacgctggtg acggtggtcg atgccagcca gttcatggcc   1726

atgctcgact ctcccgaaac cgtcgcgcgg gccgacgtca ccacggatga cagcaggcgc   1786

ccgctggccg atctgctgat cgagcaggtc gagtatgcca atgtgattct ggtcaacaaa   1846

cgcgacctgg tcgacgaggc gcagtaccag gccctgcagg cagttctcgc cgggctcaat   1906

ccaggcgcac agatcctgcc gatggtggcc ggcaacgtcg ccctgtcgag cgtccttggt   1966

acccagctgt tcgatttgcc cagccttgcc gcagcgcccg gctggatgaa acagatggac   2026

gcgcacgaca ccccggccgg cgagtcgcag acctatggcg tgacgtcatg ggtgtaccga   2086

gcgcgcgccc cgttccatcc gcaacgcttg cttgattttc tcgcccggcc ctggcgcgac   2146

ggccgtcttc tgcgcagcaa aggttatttc tggcttgcca gccgccaccg cgaaatcggc   2206
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14

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ttgctggtac acagcggcca gcagtttcaa tgggactatg ttggccattg gtggaacttc   2266

atcgacacgt cacagtggcc acaggacaag tatcgcttgc agggcatcat ggccaagtgg   2326

gacagcatcg tcggcgactg ccgacaggag ctgaaaagct tatga                   2371
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<210> 7
<211> 193
<212> PRT
<213> Pseudomonas putida

<400> 7

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Met Thr Ala Thr Ser Thr Pro Gly Glu Arg Ala Arg Ala Leu Phe Ala
1               5                  10                  15

Val Leu Lys Arg Lys Asp Leu Ile Pro Glu Gly Tyr Ile Glu Gln Leu
            20                  25                  30

Thr Gln Leu Met Glu His Gly Trp Ser Pro Glu Asn Gly Ala Arg Ile
            35                  40                  45

Val Ala Lys Ala Trp Val Asp Pro Gln Phe Arg Glu Leu Leu Leu Lys
        50                  55                  60

Asp Gly Thr Ala Ala Cys Ala Gln Phe Gly Phe Thr Gly Pro Gln Gly
65                  70                  75                  80

Glu Tyr Ile Val Ala Leu Glu Asp Thr Pro Gln Leu Lys Asn Val Ile
                85                  90                  95

Val Cys Ser Leu Cys Ser Cys Thr Asn Trp Pro Val Leu Gly Leu Pro
            100                 105                 110

Pro Glu Trp Tyr Lys Gly Phe Glu Phe Arg Ala Arg Leu Val Arg Glu
            115                 120                 125

Gly Arg Thr Val Leu Arg Glu Leu Gly Thr Glu Leu Pro Gly Asp Met
        130                 135                 140

Val Val Lys Val Trp Asp Thr Ser Ala Glu Ser Arg Tyr Leu Val Leu
145                 150                 155                 160

Pro Gln Arg Pro Ala Gly Ser Glu His Met Ser Glu Glu Gln Leu Arg
                165                 170                 175

Gln Leu Val Thr Lys Asp Val Leu Ile Gly Val Ala Leu Pro Arg Val
            180                 185                 190
```

Gly

<210>   8
<211>   220
<212>   PRT
<213>   Pseudomonas putida

<400>   8

Met Asp Gly Phe His Asp Leu Gly Gly Phe Gln Gly Phe Gly Lys Val
1   5   10   15

Pro His Arg Ile Asn Ser Leu Ser Tyr Lys Gln Val Phe Lys Gln Asp
                20   25   30

Trp Glu His Leu Ala Tyr Ser Leu Met Phe Ile Gly Val Asp His Leu
        35   40   45

Asn Lys Phe Ser Val Asp Glu Ile Arg His Ala Val Glu Arg Ile Asp
    50   55   60

Val Arg Gln His Val Gly Thr Glu Tyr Tyr Glu Arg Tyr Val Ile Ala
65   70   75   80

Thr Ala Thr Leu Leu Val Glu Thr Gly Val Ile Thr Gln Ala Glu Leu
            85   90   95

Asp Glu Ala Leu Gly Ser His Phe Lys Leu Ala Asn Pro Ala His Ala
            100   105   110

Gln Gly Arg Ala Ala Ile Ile Gly Arg Ala Pro Phe Glu Val Gly Asp
        115   120   125

Arg Val Ile Val Arg Asp Glu Tyr Val Ala Gly His Val Arg Met Pro
    130   135   140

Ala Tyr Val Arg Gly Lys Gln Gly Val Val Leu His Arg Thr Thr Glu
145   150   155   160

Gln Trp Pro Phe Pro Asp Ala Ile Gly His Gly Asp Gln Ser Ala Ala
                165   170   175

His Gln Pro Thr Tyr His Val Glu Phe Arg Val Arg Asp Leu Trp Gly
            180   185   190

16

```
         Asp Ala Ala Asp Asp Gly Leu Val Val Val Asp Leu Phe Glu Ser Tyr
             195                 200                 205


         Leu Asp Arg Val Glu Ser Pro Arg Val Val Arg Ala
             210                 215                 220



    <210>  9
    <211>  1089
    <212>  DNA
    <213>  Pseudomonas putida


    <220>
    <221>  CDS
    <222>  (1)..(1089)
    <223>  Gen der Kodierregion des Aktivatorproteins


    <400>  9
    atg agt gcc ggc gcc cag gca ggc cgg ctg ccg gtg acg gtc ctt tca        48
    Met Ser Ala Gly Ala Gln Ala Gly Arg Leu Pro Val Thr Val Leu Ser
    1               5                  10                  15

    ggc ttc ctc ggc gca ggc aag acc acc ctg ctc aac cac atc ctg cgc        96
    Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
                20                  25                  30

    aac cgc cag ggc ctg aag gtg gcg gtt atc gtc aat gac atg agc gag       144
    Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu
            35                  40                  45

    gtc aac atc gat gcc gcc cag gtc cag cgc gac gtt gcg ctg tat cgt       192
    Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
        50                  55                  60

    ggc cag gat gaa ttg ata gag atg agc aac ggc tgt atc tgc tgc acc       240
    Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
    65                  70                  75                  80

    ctg cgc gcc gac ctg ctt gag cag atc agc gcg ctg gcg cgc cag cag       288
    Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
                85                  90                  95

    cgt ttc gat tac ctg ttg atc gag tcc acc ggg att tcc gag ccg atg       336
    Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
                100                 105                 110

    cca gtc gcc gag acc ttt gcc ttt ctc gac gcc aac ggt ttc agc ctc       384
    Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
            115                 120                 125

    agc gaa ctg gcg cgg ctg gat acg ctg gtg acg gtg gtc gat gcc agc       432
    Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
        130                 135                 140

    cag ttc atg gcc atg ctc gac tct ccc gaa acc gtc gcg cgg gcc gac       480
    Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
    145                 150                 155                 160

    gtc acc acg gat gac agc agg cgc ccg ctg gcc gat ctg ctg atc gag       528
```

17

```
Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu
                165             170             175

cag gtc gag tat gcc aat gtg att ctg gtc aac aaa cgc gac ctg gtc    576
Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val
            180             185             190

gac gag gcg cag tac cag gcc ctg cag gca gtt ctc gcc ggg ctc aat    624
Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn
            195             200             205

cca ggc gca cag atc ctg ccg atg gtg gcc ggc aac gtc gcc ctg tcg    672
Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser
        210             215             220

agc gtc ctt ggt acc cag ctg ttc gat ttg ccc agc ctt gcc gca gcg    720
Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala
225             230             235             240

ccc ggc tgg atg aaa cag atg gac gcg cac gac acc ccg gcc ggc gag    768
Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu
                245             250             255

tcg cag acc tat ggc gtg acg tca tgg gtg tac cga gcg cgc gcc ccg    816
Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro
            260             265             270

ttc cat ccg caa cgc ttg ctt gat ttt ctc gcc cgg ccc tgg cgc gac    864
Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp
            275             280             285

ggc cgt ctt ctg cgc agc aaa ggt tat ttc tgg ctt gcc agc cgc cac    912
Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
        290             295             300

cgc gaa atc ggc ttg ctg gta cac agc ggc cag cag ttt caa tgg gac    960
Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp
305             310             315             320

tat gtt ggc cat tgg tgg aac ttc atc gac acg tca cag tgg cca cag   1008
Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln
                325             330             335

gac aag tat cgc ttg cag ggc atc atg gcc aag tgg gac agc atc gtc   1056
Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val
            340             345             350

ggc gac tgc cga cag gag ctg aaa agc tta tga                       1089
Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu
        355             360
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<210> 10
<211> 362
<212> PRT
<213> Pseudomonas putida

<400> 10

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Met Ser Ala Gly Ala Gln Ala Gly Arg Leu Pro Val Thr Val Leu Ser
1               5               10              15
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18

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Gly Phe Leu Gly Ala Gly Lys Thr Thr Leu Leu Asn His Ile Leu Arg
            20              25              30

Asn Arg Gln Gly Leu Lys Val Ala Val Ile Val Asn Asp Met Ser Glu
            35              40              45

Val Asn Ile Asp Ala Ala Gln Val Gln Arg Asp Val Ala Leu Tyr Arg
    50              55              60

Gly Gln Asp Glu Leu Ile Glu Met Ser Asn Gly Cys Ile Cys Cys Thr
65              70              75              80
Leu Arg Ala Asp Leu Leu Glu Gln Ile Ser Ala Leu Ala Arg Gln Gln
            85              90              95

Arg Phe Asp Tyr Leu Leu Ile Glu Ser Thr Gly Ile Ser Glu Pro Met
            100             105             110

Pro Val Ala Glu Thr Phe Ala Phe Leu Asp Ala Asn Gly Phe Ser Leu
            115             120             125

Ser Glu Leu Ala Arg Leu Asp Thr Leu Val Thr Val Val Asp Ala Ser
    130             135             140

Gln Phe Met Ala Met Leu Asp Ser Pro Glu Thr Val Ala Arg Ala Asp
145             150             155             160

Val Thr Thr Asp Asp Ser Arg Arg Pro Leu Ala Asp Leu Leu Ile Glu
            165             170             175

Gln Val Glu Tyr Ala Asn Val Ile Leu Val Asn Lys Arg Asp Leu Val
            180             185             190

Asp Glu Ala Gln Tyr Gln Ala Leu Gln Ala Val Leu Ala Gly Leu Asn
            195             200             205

Pro Gly Ala Gln Ile Leu Pro Met Val Ala Gly Asn Val Ala Leu Ser
    210             215             220

Ser Val Leu Gly Thr Gln Leu Phe Asp Leu Pro Ser Leu Ala Ala Ala
225             230             235             240

Pro Gly Trp Met Lys Gln Met Asp Ala His Asp Thr Pro Ala Gly Glu
            245             250             255

Ser Gln Thr Tyr Gly Val Thr Ser Trp Val Tyr Arg Ala Arg Ala Pro
```

19

                    260   265   270

    Phe His Pro Gln Arg Leu Leu Asp Phe Leu Ala Arg Pro Trp Arg Asp
            275   280   285

    Gly Arg Leu Leu Arg Ser Lys Gly Tyr Phe Trp Leu Ala Ser Arg His
        290   295   300

    Arg Glu Ile Gly Leu Leu Val His Ser Gly Gln Gln Phe Gln Trp Asp
    305   310   315   320

    Tyr Val Gly His Trp Trp Asn Phe Ile Asp Thr Ser Gln Trp Pro Gln
                325   330   335
    Asp Lys Tyr Arg Leu Gln Gly Ile Met Ala Lys Trp Asp Ser Ile Val
            340   345   350

    Gly Asp Cys Arg Gln Glu Leu Lys Ser Leu
            355   360

    <210> 11
    <211> 30
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Primer 1F

    <400> 11
    ctccaccata tgagtacagc tacttcaacg   30

    <210> 12
    <211> 30
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Primer 1R

    <400> 12
    cttcataagc ttctatctcg gatcaaatgg   30

    <210> 13
    <211> 25
    <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Primer 2F

    <400> 13
    atgacggcaa cttcaacccc tggtg   25

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<210>  14
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer 2R

<400>  14
tcagctcctg tcggcagtcg                                                    20
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